

## SEQUENCE LISTING

&lt;110&gt; Max Planck Gesellschaft zur Förderung der Wissensc

&lt;120&gt; Substance binding human IgG Fc receptor IIb

&lt;130&gt; 30287P-EP

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 11

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 1

Ala	Pro	Pro	Lys	Ala	Val	Leu	Lys	Leu	Glu	Pro	Pro	Trp	Ile	Asn	Val
1				5					10					15	

Leu	Gln	Glu	Asp	Ser	Val	Thr	Leu	Thr	Cys	Gln	Gly	Ala	Arg	Ser	Pro
			20					25					30		

Glu	Ser	Asp	Ser	Ile	Gln	Trp	Phe	His	Asn	Gly	Asn	Leu	Ile	Pro	Thr
		35					40					45			

His	Thr	Gln	Pro	Ser	Tyr	Arg	Phe	Lys	Ala	Asn	Asn	Asn	Asp	Ser	Gly
	50					55					60				

Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp	Pro	Val	His
65					70					75					80

Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro	His	Leu	Glu
			85					90						95	

Phe	Gln	Glu	Gly	Glu	Thr	Ile	Met	Leu	Arg	Cys	His	Ser	Trp	Lys	Asp
		100						105					110		

Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys	Ser	Gln	Lys
		115					120					125			

Phe	Ser	Arg	Leu	Asp	Pro	Thr	Phe	Ser	Ile	Pro	Gln	Ala	Asn	His	Ser
	130					135					140				

His	Ser	Gly	Asp	Tyr	His	Cys	Thr	Gly	Asn	Ile	Gly	Tyr	Thr	Leu	Phe
145					150					155					160

Ser	Ser	Lys	Pro	Val	Thr	Ile	Thr	Val	Gln	Val	Pro
			165						170		

&lt;210&gt; 2

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val

1	5	10	15
Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro	20	25	30
Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr	35	40	45
His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly	50	55	60
Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His	65	70	75
Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu	85	90	95
Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp	100	105	110
Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys	115	120	125
Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser	130	135	140
His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr	145	150	155
Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro	165	170	

<210> 3  
 <211> 13  
 <212> PRT  
 <213> Human

<400> 3  
 Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly  
 1 5 10

<210> 4  
 <211> 312  
 <212> DNA  
 <213> hybridoma

<220>  
 <221> CDS  
 <222> (1)..(312)

aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga	48
Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly	
1 5 10 15	
gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac	96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr	
20 25 30	

gtg cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct tca 48  
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser  
1 5 10 15

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gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat   96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
                20                      25                      30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga   144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
                35                      40                      45

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag   192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
                50                      55                      60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg   240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
                65                      70                      75                      80

ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat   288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
                85                      90                      95

ggt ccg ttt gct tac tgg ggc caa                               312
Gly Pro Phe Ala Tyr Trp Gly Gln
                100

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<210> 7  
 <211> 104  
 <212> PRT  
 <213> hybridoma

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<400> 7
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
  1                      5                      10                      15

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
                20                      25                      30

Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
                35                      40                      45

Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
                50                      55                      60

Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
                65                      70                      75                      80

Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
                85                      90                      95

Gly Pro Phe Ala Tyr Trp Gly Gln
                100

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<210> 8  
 <211> 331  
 <212> DNA  
 <213> hybridoma

<220>  
 <221> CDS  
 <222> (1)..(330)

&lt;400&gt; 8

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aga att cag ctg acc cag tct cct gct tcc tta gct gta tct ctg ggg      48
Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
  1             5             10             15

cag agg gcc acc atc tca tac agg gcc agc aaa agt gtc agt aca tct      96
Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
          20             25             30

ggc tat agt tat atg cac tgg aac caa cag aaa cca gga cag cca ccc      144
Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
          35             40             45

aga ctc ctc atc tat ctt gta tcc aac cta gaa tct ggg gtc cct gcc      192
Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
          50             55             60

agg ttc agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat      240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
          65             70             75             80

cct gtg gag gag gag gat gct gca acc tat tac tgt cag cac att agg      288
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
          85             90             95

gag ctt aca cgt tcg gag ggg gga cca agc tgg aga tct aac a          331
Glu Leu Thr Arg Ser Glu Gly Gly Pro Ser Trp Arg Ser Asn
          100             105             110

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&lt;210&gt; 9

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; hybridoma

&lt;400&gt; 9

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Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
  1             5             10             15

Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
          20             25             30

Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
          35             40             45

Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
          50             55             60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
          65             70             75             80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
          85             90             95

Glu Leu Thr Arg Ser Glu Gly Gly Pro Ser Trp Arg Ser Asn
          100             105             110

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&lt;210&gt; 10

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; hybridoma

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(342)

&lt;400&gt; 10

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gtg cag ctg cag gag tct gga cct ggc ctg gtg gcg ccc tca cag agc 48
Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
  1              5              10              15

ctg tcc atc aca tgc acc gtc tca ggg ttc tca tta act agc tat ggt 96
Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly
              20              25              30

gta cac tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gta 144
Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val
              35              40              45

gtg ata tgg agt gat gga agc aca acc tat aat tca gct ctc aaa tcc 192
Val Ile Trp Ser Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser
  50              55              60

aga ctg agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa 240
Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
  65              70              75              80

atg aac agt ctc caa act gat gac aca gcc atg tac tac tgt gcc aga 288
Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
              85              90              95

gag cct ccc acg acg tac gtt tgc tta ctg ggg cca agg gac cac tct 336
Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser
              100              105              110

aga tta a 343
Arg Leu

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&lt;210&gt; 11

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; hybridoma

&lt;400&gt; 11

```

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
  1              5              10              15

Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly
              20              25              30

Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val
              35              40              45

Val Ile Trp Ser Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser
  50              55              60

Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
  65              70              75              80

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
              85              90              95

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Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser  
100 105 110

Arg Leu